

SEQUENCE LISTING

<110> SmithKline Beecham Biologicals S.A.

<120> Novel compounds

<130> BM45394

<160> 6

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 969

<212> DNA

<213> *Moraxella catarrhalis*

<400> 1

atgactgtga cgatagcaat caattcacaa aatcaaaaac ccatcaagcg attgggcttg	60
atTTTTggtg tgatcaccac ttgcattttg gcaggatgtg ccagtaagcc aacctataat	120
agtacctcag gttcgggagcag tcatcgctact tcagggttcag gtggtttggc aatagggttca	180
cagggttatca cggacagtca gggcgctacca aatcgctatc aggtgaagca gggcgatact	240
gtcagtaaga ttgctcagcg ttatggatta aattggcggtg agattggaca cattaataat	300
ctaaatagca gttatacgat ttatacaggt caatggctga ctttatggtc aggtgatctc	360
aagggtgcgtg agcgtagtat cagctctggt gtgaatacag ctcacacacc ttgcgctgtg	420
gcggttcagt caagcagacc accagtacag cagcatcctg ccgtacaaaa acccacgcca	480
cctggttggtg tggtaaaaaa acccacaccg actccgctg tggttcagca gccagcacca	540
gttgccccac cagtgcagaga agcaccattt gccacgggta gctcaggggt gatgcaattt	600
cgctatcctg ttggtgcgac caatccagtg gttcgacgct ttggtacggc gacagtggcc	660
ggctcaactg ttaccagtaa tggcatgtgg ttttctggac gagatggcga ttaattaac	720
gccagtaatg caggcacagt cattcaagct gatcacaata tggacggggc gagtattgtg	780
attcagcata ccaatggatt tgtttcaagc tatatccata ttaaggacgc tcaagttaaa	840
acaggcgata cgggtgcgtac cggtcagcgt attgcaagca tgaaaaatca gccaacgggt	900
gcggcactat ttgaatttag aatttctaga aatggcggtg atgttgatcc attgacagta	960
cttaaatag	969

<210> 2

<211> 322

<212> PRT

<213> *Moraxella catarrhalis*

<400> 2

```

Met Thr Val Thr Ile Ala Ile Asn Ser Gln Asn Gln Lys Pro Ile Lys
 1           5           10           15
Arg Leu Gly Leu Ile Phe Gly Val Ile Thr Thr Cys Ile Leu Ala Gly
 20           25           30
Cys Ala Ser Lys Pro Thr Tyr Asn Ser Thr Ser Gly Ser Gly Ser His
 35           40           45
Arg Thr Ser Gly Ser Gly Gly Leu Ala Ile Gly Ser Gln Val Ile Thr
 50           55           60
Asp Ser Gln Gly Val Pro Asn Arg Tyr Gln Val Lys Gln Gly Asp Thr
 65           70           75           80
Val Ser Lys Ile Ala Gln Arg Tyr Gly Leu Asn Trp Arg Glu Ile Gly
 85           90           95
His Ile Asn Asn Leu Asn Ser Ser Tyr Thr Ile Tyr Thr Gly Gln Trp
100           105           110
Leu Thr Leu Trp Ser Gly Asp Leu Lys Val Arg Glu Arg Ser Ile Ser
115           120           125
Ser Gly Val Asn Thr Ala His Thr Pro Ser Pro Val Ala Val Gln Ser
130           135           140
Ser Arg Pro Pro Val Gln Gln His Pro Ala Val Gln Lys Pro Thr Pro
145           150           155           160
Pro Val Val Val Val Lys Lys Pro Thr Pro Thr Pro Pro Val Val Gln
165           170           175
Gln Pro Ala Pro Val Ala Pro Pro Val Thr Glu Ala Pro Phe Ala Thr
180           185           190
Gly Ser Ser Gly Val Met Gln Phe Arg Tyr Pro Val Gly Ala Thr Asn
195           200           205
Pro Val Val Arg Arg Phe Gly Thr Ala Thr Val Ala Gly Ser Thr Val
210           215           220
Thr Ser Asn Gly Met Trp Phe Ser Gly Arg Asp Gly Asp Leu Ile Asn
225           230           235           240
Ala Ser Asn Ala Gly Thr Val Ile Gln Ala Asp His Asn Met Asp Gly
245           250           255
Ala Ser Ile Val Ile Gln His Thr Asn Gly Phe Val Ser Ser Tyr Ile
260           265           270
His Ile Lys Asp Ala Gln Val Lys Thr Gly Asp Thr Val Arg Thr Gly
275           280           285

```

Gln Arg Ile Ala Ser Met Lys Asn Gln Pro Ser Gly Ala Ala Leu Phe
 290 295 300
 Glu Phe Arg Ile Ser Arg Asn Gly Val Tyr Val Asp Pro Leu Thr Val
 305 310 315 320
 Leu Lys

<210> 3
 <211> 966
 <212> DNA
 <213> *Moraxella catarrhalis*

<400> 3

atgactgtga cgatagcaat caattcacaa aatcaaaaac ccatcaagcg attgggcttg 60
 atttttggtg tgatcaccac ttgcattttg gcaggatgtg ccagtaagcc aacctataat 120
 agtacctcag gttcgggcag tcatcgact tcaggttcag gtggtttggc aatagggttca 180
 caggttatca cggacagtca gggcgtagca aatcgctatc aggtgaagca gggcgatact 240
 gtcagtaaga ttgctcagcg ttatggatta aattggcgtg agattggaca cattaataat 300
 ctaaataagcg gttatacgat ttatacaggt caatggctga ctttatggtc aggtgatctc 360
 aagggtgcgtg agcgtagtat cagctctggg gtgaatacag ctcacacacc ttgcgctgtg 420
 gcggttcagt caagcagacc accagtacag cagcatcctg ccgtacaaaa acccacgcca 480
 cctggttgtg tggtaaaaaa acccacaccg actcgcgctg tggttcagca gccagcacca 540
 gttgccccac cagtgcagca agcaccattt gccacgggta gtcaggggt gatgcaattt 600
 cgctatcctg ttggtgcgac caatccagtg gttcgacgct ttggtacggc gacagtggcc 660
 ggctcaactg ttaccagtaa tggcatgtgg ttttctggac gagatggcga ttttaattaac 720
 gccagtaatg caggcacagt cattcaagct gatcacaata tggacggggc gagtattgtg 780
 attcagcata ccaatggatt tgtttcaagc tatatccata ttaaggacgc tcaagttaa 840
 acaggcgata cgggtgcgtac cggtcagcgt attgcaagca tgaaaaatca gccaagcgg 900
 gcggcactat ttgaatttag aatttctaga aatggcgtgt atgttgatcc attgacagta 960
 cttaaa 966

<210> 4
 <211> 322
 <212> PRT
 <213> *Moraxella catarrhalis*

<400> 4

Met Thr Val Thr Ile Ala Ile Asn Ser Gln Asn Gln Lys Pro Ile Lys
 1 5 10 15
 Arg Leu Gly Leu Ile Phe Gly Val Ile Thr Thr Cys Ile Leu Ala Gly

20 25 30
 Cys Ala Ser Lys Pro Thr Tyr Asn Ser Thr Ser Gly Ser Gly Ser His
 35 40 45
 Arg Thr Ser Gly Ser Gly Gly Leu Ala Ile Gly Ser Gln Val Ile Thr
 50 55 60
 Asp Ser Gln Gly Val Pro Asn Arg Tyr Gln Val Lys Gln Gly Asp Thr
 65 70 75 80
 Val Ser Lys Ile Ala Gln Arg Tyr Gly Leu Asn Trp Arg Glu Ile Gly
 85 90 95
 His Ile Asn Asn Leu Asn Ser Gly Tyr Thr Ile Tyr Thr Gly Gln Trp
 100 105 110
 Leu Thr Leu Trp Ser Gly Asp Leu Lys Val Arg Glu Arg Ser Ile Ser
 115 120 125
 Ser Gly Val Asn Thr Ala His Thr Pro Ser Pro Val Ala Val Gln Ser
 130 135 140
 Ser Arg Pro Pro Val Gln Gln His Pro Ala Val Gln Lys Pro Thr Pro
 145 150 155 160
 Pro Val Val Val Val Lys Lys Pro Thr Pro Thr Pro Pro Val Val Gln
 165 170 175
 Gln Pro Ala Pro Val Ala Pro Pro Val Thr Glu Ala Pro Phe Ala Thr
 180 185 190
 Gly Ser Ser Gly Val Met Gln Phe Arg Tyr Pro Val Gly Ala Thr Asn
 195 200 205
 Pro Val Val Arg Arg Phe Gly Thr Ala Thr Val Ala Gly Ser Thr Val
 210 215 220
 Thr Ser Asn Gly Met Trp Phe Ser Gly Arg Asp Gly Asp Leu Ile Asn
 225 230 235 240
 Ala Ser Asn Ala Gly Thr Val Ile Gln Ala Asp His Asn Met Asp Gly
 245 250 255
 Ala Ser Ile Val Ile Gln His Thr Asn Gly Phe Val Ser Ser Tyr Ile
 260 265 270
 His Ile Lys Asp Ala Gln Val Lys Thr Gly Asp Thr Val Arg Thr Gly
 275 280 285
 Gln Arg Ile Ala Ser Met Lys Asn Gln Pro Ser Gly Ala Ala Leu Phe
 290 295 300
 Glu Phe Arg Ile Ser Arg Asn Gly Val Tyr Val Asp Pro Leu Thr Val
 305 310 315 320
 Leu Lys

<210> 5

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 5

aggcagaggc atatgactgt gacgatagca atcaa

35

<210> 6

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 6

aggcagaggc tcgagtttaa gtactgtcaa tggatcaaca ta

42